Phyre^2

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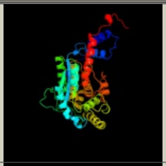
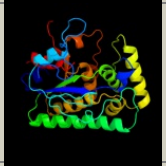
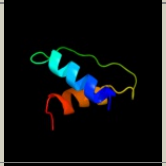
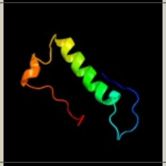
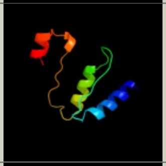
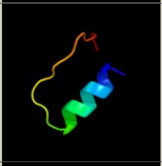
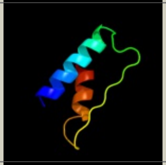
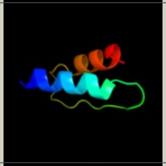
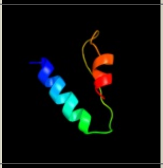
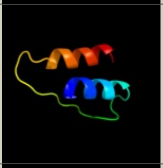
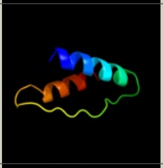
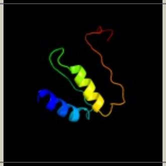
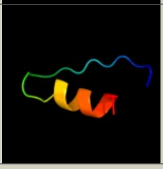
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l5oa_	Alignment		100.0	79	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
2	d1j33a_	Alignment		100.0	39	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
3	c3l0zC_	Alignment		100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative nicotinate-nucleotide-dimethylbenzimidazole **PDBTitle:** crystal structure of a putative nicotinate-nucleotide-2 dimethylbenzimidazole phosphoribosyltransferase from3 methanocaldococcus jannaschii dsm 2661
4	c3u4gA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**namn:dmb phosphoribosyltransferase; **PDBTitle:** the structure of cobt from pyrococcus horikoshii
5	d1htwa_	Alignment		69.7	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
6	c3lmaC_	Alignment		50.2	23	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**stage v sporulation protein ad (spovad); **PDBTitle:** crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
7	c2c99A_	Alignment		45.2	17	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**psp operon transcriptional activator; **PDBTitle:** structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
8	c2re2A_	Alignment		40.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein ta1041; **PDBTitle:** crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
9	c2c9oC_	Alignment		33.5	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
10	c1ojlF_	Alignment		32.6	15	**PDB header:**response regulator **Chain:** F: **PDB Molecule:**transcriptional regulatory protein zrar; **PDBTitle:** crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
11	c3k6jA_	Alignment		30.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans

12	d2tpta2	Alignment		30.2	19	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
13	c3co5B_	Alignment		30.0	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative two-component system transcriptional response **PDBTitle:** crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
14	c3tqfA_	Alignment		28.7	13	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**hpr(ser) kinase; **PDBTitle:** structure of the hpr(ser) kinase/phosphatase from coxiella burnetii
15	d1g6oa_	Alignment		27.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
16	d1l8qa2	Alignment		26.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
17	d1ixsb2	Alignment		25.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
18	c3fdiA_	Alignment		24.5	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
19	d1ny5a2	Alignment		24.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
20	d1kkma_	Alignment		24.0	21	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**HPr kinase HprK C-terminal domain
21	c2qmhK_	Alignment	not modelled	23.9	21	**PDB header:**transferase **Chain:** K: **PDB Molecule:**hpr kinase/phosphorylase; **PDBTitle:** structure of v267f mutant hprk/p
22	d2fywa1	Alignment	not modelled	23.8	10	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
23	c1hqcB_	Alignment	not modelled	23.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
24	d1ko7a2	Alignment	not modelled	22.6	21	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**HPr kinase HprK C-terminal domain
25	d1g41a_	Alignment	not modelled	22.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
26	c2vhiG_	Alignment	not modelled	22.0	20	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cg3027-pa; **PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
27	c2gx8B_	Alignment	not modelled	21.6	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3
28	c2zktB_	Alignment	not modelled	21.4	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
						PDB header:transferase

29	c3h5qA_	Alignment	not modelled	20.9	16	**Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
30	d1byia_	Alignment	not modelled	20.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
31	c3pfiB_	Alignment	not modelled	20.8	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction atp-dependent dna helicase ruvb; **PDBTitle:** 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
32	c2gzaB_	Alignment	not modelled	20.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**type iv secretion system protein virb11; **PDBTitle:** crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
33	c2dsjA_	Alignment	not modelled	18.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
34	d2gx8a1	Alignment	not modelled	18.3	14	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
35	c3b5qB_	Alignment	not modelled	18.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
36	c1otpA_	Alignment	not modelled	17.6	17	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
37	d1qvra2	Alignment	not modelled	17.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
38	d1y63a_	Alignment	not modelled	17.1	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
39	c3dtpA_	Alignment	not modelled	17.0	13	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
40	d1d2na_	Alignment	not modelled	16.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
41	d1ye8a1	Alignment	not modelled	16.8	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
42	c2qzuA_	Alignment	not modelled	16.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
43	c3ed4A_	Alignment	not modelled	16.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
44	c2w8dB_	Alignment	not modelled	16.3	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid synthase 2; **PDBTitle:** distinct and essential morphogenic functions for wall- and2 lipo-teichoic acids in bacillus subtilis
45	d1m8pa3	Alignment	not modelled	16.2	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
46	c2qgzA_	Alignment	not modelled	15.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative primosome component; **PDBTitle:** crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
47	d1knxa2	Alignment	not modelled	15.5	22	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**HPr kinase HprK C-terminal domain
48	c3mogA_	Alignment	not modelled	15.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
49	c3ec2A_	Alignment	not modelled	15.3	24	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication protein dnac; **PDBTitle:** crystal structure of the dnac helicase loader
50	d1uoua2	Alignment	not modelled	15.2	19	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
51	c2nydB_	Alignment	not modelled	15.0	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0135 protein sa1388; **PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388
						Fold:P-loop containing nucleoside triphosphate hydrolases

52	d1a5ta2	Alignment	not modelled	15.0	18	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
53	d1brwa2	Alignment	not modelled	14.9	22	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
54	d1hdha_	Alignment	not modelled	14.6	8	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
55	d1nmpa_	Alignment	not modelled	14.4	27	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
56	c2bpqB_	Alignment	not modelled	14.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
57	c1ko7B_	Alignment	not modelled	14.2	22	**PDB header:**transferase,hydrolase **Chain:** B: **PDB Molecule:**hpr kinase/phosphatase; **PDBTitle:** x-ray structure of the hpr kinase/phosphatase from2 staphylococcus xylosus at 1.95 a resolution
58	c2w5tA_	Alignment	not modelled	14.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
59	c3lxqB_	Alignment	not modelled	13.9	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp1736; **PDBTitle:** the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
60	c2oaq1_	Alignment	not modelled	13.7	25	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**type ii secretion system protein; **PDBTitle:** crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
61	d1p49a_	Alignment	not modelled	13.5	20	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
62	d2i09a1	Alignment	not modelled	13.4	36	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
63	d2cvoa1	Alignment	not modelled	13.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
64	d1m7gb_	Alignment	not modelled	12.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
65	d1r6bx2	Alignment	not modelled	12.9	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
66	c3e2vA_	Alignment	not modelled	12.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
67	d1jbka_	Alignment	not modelled	12.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
68	c2qmoA_	Alignment	not modelled	12.6	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
69	d1o0sa2	Alignment	not modelled	12.5	24	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
70	d1qzxa3	Alignment	not modelled	12.5	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
71	d1in4a2	Alignment	not modelled	12.3	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
72	d1uf5a_	Alignment	not modelled	12.0	15	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
73	d1fsua_	Alignment	not modelled	12.0	21	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
74	c2p65A_	Alignment	not modelled	11.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf08_0063; **PDBTitle:** crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
75	d1g8fa3	Alignment	not modelled	11.8	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
76	c3nwjB_	Alignment	not modelled	11.6	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atsk2; **PDBTitle:** crystal structure of shikimate kinase from arabidopsis thaliana2 (atsk2)
77	c1knxF_	Alignment	not modelled	11.3	23	**PDB header:**transferase/hydrolase **Chain:** F: **PDB Molecule:**probable hpr(ser) kinase/phosphatase; **PDBTitle:** hpr kinase/phosphatase from mycoplasma pneumoniae

78	c1brwB_	Alignment	not modelled	11.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
79	c3hdtB_	Alignment	not modelled	10.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase from clostridium symbiosum atcc2 14940
80	d1j31a_	Alignment	not modelled	10.7	19	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
81	d1auka_	Alignment	not modelled	10.7	30	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
82	d2i3ba1	Alignment	not modelled	10.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
83	c2chvE_	Alignment	not modelled	10.6	29	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
84	c3n4pA_	Alignment	not modelled	10.4	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**terminase subunit ul89 protein; **PDBTitle:** human cytomegalovirus terminase nuclease domain
85	d1g64b_	Alignment	not modelled	10.3	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
86	c3labA_	Alignment	not modelled	10.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate); **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
87	d1p5ja_	Alignment	not modelled	10.2	20	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
88	c1p5jA_	Alignment	not modelled	10.2	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
89	c3m8yC_	Alignment	not modelled	10.0	36	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
90	c3ab8B_	Alignment	not modelled	9.9	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein ttha0350; **PDBTitle:** crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
91	d2fzva1	Alignment	not modelled	9.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
92	d1t35a_	Alignment	not modelled	9.8	28	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
93	c2q4dB_	Alignment	not modelled	9.8	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
94	d1g5ta_	Alignment	not modelled	9.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
95	c3n4qA_	Alignment	not modelled	9.5	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**terminase subunit ul89 protein; **PDBTitle:** human cytomegalovirus terminase nuclease domain, mn soaked
96	d2ieaa3	Alignment	not modelled	9.4	14	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
97	c2we7A_	Alignment	not modelled	9.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
98	c2i09A_	Alignment	not modelled	9.1	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
99	c2px0D_	Alignment	not modelled	9.1	23	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)